

SEQUENCE LISTING

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Burlingame, Alma L.  
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Walker, Craig  
Watkins, Maren  
Shetty, Reshma  
Cruz, Lourdes J.  
Imperial, Julita  
Colledge, Clark  
University of Utah Research Foundation  
Vrije Universiteit  
Regents of the University of California
- <120> Gamma-Conopeptides
- <130> Gamma-Conpeptides
- <140>  
<141>
- <150> US 60/069,706  
<151> 1997-12-16
- <160> 47
- <170> PatentIn Ver. 2.0
- <210> 1  
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<213> Artificial Sequence
- <220>  
<223> Description of Artificial Sequence:generic formula  
of gamma-conopeptides
- <220>  
<221> PEPTIDE  
<222> (1)  
<223> Xaa at residue 1 is des-Xaa or a peptide having  
1-6 amino acids.
- <220>  
<221> PEPTIDE  
<222> (3)  
<223> Xaa at residue 3 is a peptide having 5-6 amino  
acids.
- <220>  
<221> PEPTIDE  
<222> (5)  
<223> Xaa at residue 5 is a peptide having 4 amino  
acids.
- <220>  
<221> PEPTIDE  
<222> (6)  
<223> Xaa at residue 6 is Glu, gamma-carboxylglutamate  
or Gln.
- <220>

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<221> PEPTIDE  
 <222> (9)  
 <223> Xaa at residue 9 is a peptide having 3-4 amino acids.

<220>  
 <221> PEPTIDE  
 <222> (11)  
 <223> Xaa at residue 11 is a peptide having 3-6 amino acids.

<220>  
 <221> PEPTIDE  
 <222> (13)  
 <223> Xaa at residue 13 is des-Xaa or a peptide of 2-9 amino acids.

<400> 1  
 Xaa Cys Xaa Cys Xaa Xaa Cys Cys Xaa Cys Xaa Cys Xaa  
     1                    5                    10

<210> 2  
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<220>  
 <223> Description of Artificial Sequence:generic sequence of gamma-conopeptides.

<220>  
 <221> PEPTIDE  
 <222> (1)  
 <223> Xaa at residue 1 is des-Xaa or a peptide having 1-6 amino acids.

<220>  
 <221> PEPTIDE  
 <222> (3)  
 <223> Xaa at residue 3 is a peptide having 5-6 amino acids.

<220>  
 <221> PEPTIDE  
 <222> (5)  
 <223> Xaa at residue 5 is a peptide having 4 amino acids.

<220>  
 <221> PEPTIDE  
 <222> (6)  
 <223> Xaa at residue 6 is Glu, gamma-carboxyglutamate or Gln.

<220>  
 <221> PEPTIDE  
 <222> (9)  
 <223> Xaa at residue 9 is Ser or Thr.

<220>  
 <221> PEPTIDE  
 <222> (10)  
 <223> Xaa at residue 10 is a peptide having 2-3 amino

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acids.

<220>  
 <221> PEPTIDE  
 <222> (12)  
 <223> Xaa at residue 12 is a peptide having 3-6 amino acids.

<220>  
 <221> PEPTIDE  
 <222> (14)  
 <223> Xaa at residue 14 is a peptide having 2-9 amino acids.

<400> 2  
 Xaa Cys Xaa Cys Xaa Xaa Cys Cys Xaa Xaa Cys Xaa Cys Xaa  
 1 5 10

<210> 3  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:generic formula of gamma-conopeptides

<220>  
 <221> PEPTIDE  
 <222> (1)  
 <223> Xaa at residue 1 is a peptide having 1-6 amino acids.

<220>  
 <221> PEPTIDE  
 <222> (3)  
 <223> Xaa at residue 3 is a hexapeptide.

<220>  
 <221> PEPTIDE  
 <222> (5)  
 <223> Xaa at residue 5 is a peptide having 4 amino acids.

<220>  
 <221> PEPTIDE  
 <222> (6)  
 <223> Xaa at residue 6 is Glu or gamma-carboxyglutamate.

<220>  
 <221> PEPTIDE  
 <222> (14)  
 <223> Xaa at residue 14 is a tripeptide.

<220>  
 <221> PEPTIDE  
 <222> (16)  
 <223> Xaa at residue 16 is a peptide having 7-9 amino acids.

<400> 3  
 Xaa Cys Xaa Cys Xaa Xaa Cys Cys Ser Asn Ser Cys Asp Xaa Cys Xaa  
 1 5 10 15

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<210> 4  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:generic  
sequence of gamma-conopeptides.

<220>  
<221> PEPTIDE  
<222> (1)  
<223> Xaa at residue 1 is a peptide having 1-6 amino  
acids.

<220>  
<221> PEPTIDE  
<222> (3)  
<223> Xaa at residue 3 is a hexapeptide.

<220>  
<221> PEPTIDE  
<222> (5)  
<223> Xaa at residue 5 is Ser or Thr.

<220>  
<221> PEPTIDE  
<222> (6)  
<223> Xaa at residue 6 is a tripeptide.

<220>  
<221> PEPTIDE  
<222> (7)  
<223> Xaa at residue 7 is Glu or gamma-carboxyglutamate.

<220>  
<221> PEPTIDE  
<222> (15)  
<223> Xaa at residue 15 is a tripeptide.

<220>  
<221> PEPTIDE  
<222> (17)  
<223> Xaa at residue is a peptide having 7-9 amino  
acids.

<400> 4  
Xaa Cys Xaa Cys Xaa Xaa Xaa Cys Cys Ser Asn Ser Cys Asp Xaa Cys  
1 5 10 15

Xaa

<210> 5  
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<220>  
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sequence of gamma-conopeptides.

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<220>
<221> -PEPTIDE - - - - -
<222> (1)..(31)
<223> Xaa at residue 5 is Trp or 6-bromo-Trp; Xaa at

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residues 14 and 26 are Glu or  
gamma-carboxyglutamate; Xaa at residue 31 is Pro  
or hydroxy-Pro.

<400> 6  
Asp Cys Thr Ser Xaa Phe Gly Arg Cys Thr Val Asn Ser Xaa Cys Cys  
1 5 10 15  
Ser Asn Ser Cys Asp Gln Thr Tyr Cys Xaa Leu Tyr Ala Phe Xaa Ser  
20 25 30

<210> 7  
<211> 34  
<212> PRT  
<213> Conus textile

<220>  
<221> PEPTIDE  
<222> (1)..(34)  
<223> Xaa at residues 1, 7 and 34 are Trp or  
6-bromo-Trp; Xaa at residues 3 and 16 are Glu or  
gamma-carboxyglutamate; Xaa at residues 31 and 32  
are Pro or hydroxy-Pro.

<400> 7  
Xaa Leu Xaa Cys Ser Val Xaa Phe Ser His Cys Thr Lys Asp Ser Xaa  
1 5 10 15  
Cys Cys Ser Asn Ser Cys Asp Gln Thr Tyr Cys Thr Leu Met Xaa Xaa  
20 25 30  
Asp Xaa

<210> 8  
<211> 39  
<212> PRT  
<213> Conus textile

<220>  
<221> PEPTIDE  
<222> (1)..(39)  
<223> Xaa at residues 1, 2, 4, 10 and 39 are Trp or  
6-bromo-Trp ; Xaa at residues 19 and 31 are Glu or  
gamma-carboxyglutamate; Xaa at residues 34, 36 and  
37 are Pro or hydroxy-Pro.

<400> 8  
Xaa Xaa Arg Xaa Gly Gly Cys Met Ala Xaa Phe Gly Leu Cys Ser Arg  
1 5 10 15  
Asp Ser Xaa Cys Cys Ser Asn Ser Cys Asp Val Thr Arg Cys Xaa Leu  
20 25 30  
Met Xaa Phe Xaa Xaa Asp Xaa  
35

<210> 9

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<211> 27  
 <212> PRT  
 <213> Conus textile

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residues 9, 13 and 17 are Glu or  
 gamma-carboxyglutamate.

<400> 9  
 Cys Lys Thr Tyr Ser Lys Tyr Cys Xaa Ala Asp Ser Xaa Cys Cys Thr  
 1 5 10 15

Xaa Gln Cys Val Arg Ser Tyr Cys Thr Leu Phe  
 20 25

<210> 10  
 <211> 34  
 <212> PRT  
 <213> Conus textile

<220>  
 <221> PEPTIDE  
 <222> (1)..(34)  
 <223> Xaa at residues 2, 3, 10 and 32 are Trp or  
 6-bromo-Trp; Xaa at residues 18, 26 and 33 are Glu  
 or gamma-carboxyglutamate; Xaa at residue 12 is  
 Pro or hydroxy-Pro.

<400> 10  
 Asp Xaa Xaa Asp Asp Gly Cys Ser Val Xaa Gly Xaa Cys Thr Tyr Asn  
 1 5 10 15

Ala Xaa Cys Cys Ser Gly Asp Cys His Xaa Thr Cys Ile Phe Gly Xaa  
 20 25 30

Xaa Val

<210> 11  
 <211> 31  
 <212> PRT  
 <213> Conus textile

<220>  
 <221> PEPTIDE  
 <222> (1)..(31)  
 <223> Xaa at residues 3 and 31 are Trp of 6-bromo-Trp;  
 Xaa at residues 5, 18, 22 and 25 are Glu or  
 gamma-carboxyglutamate; Xaa at residue 16 is Pro  
 or hydroxy-Pro.

<400> 11  
 Gly Met Xaa Gly Xaa Cys Lys Asp Gly Leu Thr Thr Cys Leu Ala Xaa  
 1 5 10 15

Ser Xaa Cys Cys Ser Xaa Asp Cys Xaa Gly Ser Cys Thr Met Xaa  
 20 25 30

<210> 12

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<211> 32  
<212> PRT  
<213> Conus gloriamaris

<220>  
<221> PEPTIDE  
<222> (1)..(32)  
<223> Xaa at residue 5 is Trp or 6-bromo-Trp; Xaa at residue 1 is Glu or gamma-carboxyglutamate; Xaa at residues 8 and 11 are Pro or hydroxy-Pro.

<400> 12  
Xaa Cys Arg Ala Xaa Tyr Ala Xaa Cys Ser Xaa Gly Ala Gln Cys Cys  
1 5 10 15  
Ser Leu Leu Met Cys Ser Lys Ala Thr Ser Arg Cys Ile Leu Ala Leu  
20 25 30

<210> 13  
<211> 29  
<212> PRT  
<213> Conus marmoreus

<220>  
<221> PEPTIDE  
<222> (1)..(29)  
<223> Xaa at residues 8 and 15 are Trp or 6-bromo-Trp; Xaa at residues 5, 16 and 23 are Glu or gamma-carboxyglutamate; Xaa at residue 10 is Pro or hydroxy-Pro.

<400> 13  
Asn Gly Gln Cys Xaa Asp Val Xaa Met Xaa Cys Thr Ser Asn Xaa Xaa  
1 5 10 15  
Cys Cys Ser Leu Asp Cys Xaa Met Tyr Cys Thr Gln Ile  
20 25

<210> 14  
<211> 27  
<212> PRT  
<213> Conus marmoreus

<220>  
<221> PEPTIDE  
<222> (1)..(27)  
<223> Xaa at residue 4 is Trp or 6-bromo-Trp; Xaa at residues 9, 12, 13 and 17 are Glu or gamma-carboxyglutamate.

<400> 14  
Cys Gly Gly Xaa Ser Thr Tyr Cys Xaa Val Asp Xaa Xaa Cys Cys Ser  
1 5 10 15  
Xaa Ser Cys Val Arg Ser Tyr Cys Thr Leu Phe  
20 25

<210> 15

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<211> 26  
<212> PRT  
<213> Conus marmoreus

<220>  
<221> PEPTIDE  
<222> (1)..(26)  
<223> Xaa at residues 8 and 15 are Trp or 6-bromo-Trp;  
Xaa at residue 16 is Glu or  
gamma-carboxyglutamate.

<400> 15  
Asn Gly Gly Cys Lys Ala Thr Xaa Met Ser Cys Ser Ser Gly Xaa Xaa  
1 5 10 15  
Cys Cys Ser Met Ser Cys Asp Met Tyr Cys  
20 25

<210> 16  
<211> 323  
<212> DNA  
<213> Conus textile

<220>  
<221> CDS  
<222> (1)..(153)

<400> 16  
gaa cgg gct aag atc aac ttg ctt cca aag aga aag cca cct gct gag 48  
Glu Arg Ala Lys Ile Asn Leu Leu Pro Lys Arg Lys Pro Pro Ala Glu  
1 5 10 15  
cgt tgg ttg gaa tgc agt gtt tgg ttt tca cat tgt acg aag gac tcg 96  
Arg Trp Leu Glu Cys Ser Val Trp Phe Ser His Cys Thr Lys Asp Ser  
20 25 30  
gaa tgt tgt tct aat agt tgt gac caa acg tac tgc acg tta atg cca 144  
Glu Cys Cys Ser Asn Ser Cys Asp Gln Thr Tyr Cys Thr Leu Met Pro  
35 40 45  
ccg gac tgg tgacatcgcc actctcctgt tcagagtctt caaggctttt 193  
Pro Asp Trp  
50

gttctctttt gaagaatttt aacgagtga caaaaaagt gactagcatg tttccttttc 253  
cctttgcaaa atcaatgatg gaggtaaaag cctcccat tgtcttcac aataaagaac 313  
ttatcatcat 323

<210> 17  
<211> 51  
<212> PRT  
<213> Conus textile

<400> 17  
Glu Arg Ala Lys Ile Asn Leu Leu Pro Lys Arg Lys Pro Pro Ala Glu  
1 5 10 15  
Arg Trp Leu Glu Cys Ser Val Trp Phe Ser His Cys Thr Lys Asp Ser  
20 25 30

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Glu Cys Cys Ser Asn Ser Cys Asp Gln Thr Tyr Cys Thr Leu Met Pro  
35 40 45

Pro Asp Trp  
50

<210> 18  
<211> 510  
<212> DNA  
<213> Conus textile

<220>  
<221> CDS  
<222> (95)..(337)

<400> 18  
tgactcgcca tctcctctct cagtctccct gacagctgcc ttcagtcgac cctgccgtca 60  
tctcaacgca cacttgaagt gaaaaacctt tctc atg gag aaa ctg aca att ctg 115  
Met Glu Lys Leu Thr Ile Leu  
1 5

ctt ctt gtt gct gct gta ctg ttg tgg atc cag gcc cta aat caa gaa 163  
Leu Leu Val Ala Ala Val Leu Leu Ser Ile Gln Ala Leu Asn Gln Glu  
10 15 20

aaa cac caa cgg gca aag atc aac ttg ctt tca aag aga aag cca cct 211  
Lys His Gln Arg Ala Lys Ile Asn Leu Leu Ser Lys Arg Lys Pro Pro  
25 30 35

gct gag cgt tgg tgg cgg tgg gga gga tgc atg gct tgg ttt ggg ctt 259  
Ala Glu Arg Trp Trp Arg Trp Gly Gly Cys Met Ala Trp Phe Gly Leu  
40 45 50 55

tgt tgg agg gac tgg gaa tgt tgt tct aat agt tgt gac gta acg cgc 307  
Cys Ser Arg Asp Ser Glu Cys Cys Ser Asn Ser Cys Asp Val Thr Arg  
60 65 70

tgc gag tta atg cca ttc cca cca gac tgg tgacatcgac actctcctct 357  
Cys Glu Leu Met Pro Phe Pro Pro Asp Trp  
75 80

tcagagtctt caaggctttt gttctctttt gaagaatttt tacgagtga caaaaacgtg 417  
gactagcacg tttccttttc cctttgcaaa atcaatgatg gaggtaaaag tgtcccat 477  
tgtcttcctc aataaagaac ttatcatcat aat 510

<210> 19  
<211> 81  
<212> PRT  
<213> Conus textile

<400> 19  
Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Leu Ser  
1 5 10 15  
Ile Gln Ala Leu Asn Gln Glu Lys His Gln Arg Ala Lys Ile Asn Leu  
20 25 30  
Leu Ser Lys Arg Lys Pro Pro Ala Glu Arg Trp Trp Arg Trp Gly Gly  
35 40 45

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<400> 21
Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser
  1      5      10      15
Thr Gln Ala Met Phe Gln Gly Asp Gly Glu Lys Ser Arg Lys Ala Glu
      20      25      30
Ile Asn Phe Ser Glu Thr Arg Lys Leu Ala Arg Asn Lys Gln Lys Arg
    35      40      45

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Cys Lys Thr Tyr Ser Lys Tyr Cys Glu Ala Asp Ser Glu Cys Cys Thr  
50 55 60

Glu Gln Cys Val Arg Ser Tyr Cys Thr Leu Phe Gly  
65 70 75

<210> 22  
<211> 460  
<212> DNA  
<213> Conus textile

<220>  
<221> CDS  
<222> (49)..(273)

<400> 22  
ctgccgtcat ctcagcgcac acttggttaag aagtgaataa ccttgatc atg gag aaa 57  
Met Glu Lys  
1

ctg aca att ctg ctt ctt gtt gct gct gtg ctg atg tcg acc cag gcc 105  
Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser Thr Gln Ala  
5 10 15

cta att caa gat caa cgc caa aag gca aag atc aac ttg ttt tca aag 153  
Leu Ile Gln Asp Gln Arg Gln Lys Ala Lys Ile Asn Leu Phe Ser Lys  
20 25 30 35

aga cag gca tat gct cgt gat tgg tgg gac gat ggc tgc agt gtg tgg 201  
Arg Gln Ala Tyr Ala Arg Asp Trp Trp Asp Asp Gly Cys Ser Val Trp  
40 45 50

ggg cct tgt acg gtg aac gca gaa tgt tgt tct ggt gat tgt cat gaa 249  
Gly Pro Cys Thr Val Asn Ala Glu Cys Cys Ser Gly Asp Cys His Glu  
55 60 65

acg tgc att ttc ggg tgg gaa gtc tgaccacaaa ccatccgaca tcgccactct 303  
Thr Cys Ile Phe Gly Trp Glu Val  
70 75

cctcttcaga gacttcaagg cttttgttct cttttgaaga attttacgag tgagcaaaaa 363

ggtagactag cacgtttctt tttcccttg caaatcaat gatggaggta aaagcctccc 423

attttgtcct catcaataaa gaacttatca tcataat 460

<210> 23  
<211> 75  
<212> PRT  
<213> Conus textile

<400> 23  
Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser  
1 5 10 15

Thr Gln Ala Leu Ile Gln Asp Gln Arg Gln Lys Ala Lys Ile Asn Leu  
20 25 30

Phe Ser Lys Arg Gln Ala Tyr Ala Arg Asp Trp Trp Asp Asp Gly Cys  
35 40 45

Ser Val Trp Gly Pro Cys Thr Val Asn Ala Glu Cys Cys Ser Gly Asp

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50

55

60

Cys His Glu Thr Cys Ile Phe Gly Trp Glu Val  
65 70 75

<210> 24  
<211> 533  
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<213> Conus textile

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<222> (110)..(337)

<400> 24  
ctctgccggt tgacacntca tctactctct cagtctccct gacagctgcc ttcagtcgac 60  
cctgccgtca tctcagcgca gacttgataa gaagtgaata acctttatc atg gag aaa 118  
Met Glu Lys  
1

ctg aca atc ctg ctt ctt gtt gct gct gta ctg atg tcg acc cag gcc 166  
Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser Thr Gln Ala  
5 10 15

ctg gtt gaa cgt gct gga gaa aac cac tca aag gag aac atc aat ttt 214  
Leu Val Glu Arg Ala Gly Glu Asn His Ser Lys Glu Asn Ile Asn Phe  
20 25 30 35

tta tta aaa aga aag aga gct gct gac agg ggg atg tgg ggc gaa tgc 262  
Leu Leu Lys Arg Lys Arg Ala Ala Asp Arg Gly Met Trp Gly Glu Cys  
40 45 50

aaa gat ggg tta acg aca tgt ttg gcg ccc tca gag tgt tgt tct gag 310  
Lys Asp Gly Leu Thr Thr Cys Leu Ala Pro Ser Glu Cys Cys Ser Glu  
55 60 65

gat tgt gaa ggg agc tgc acg atg tgg tgatgaattc tgaccacaag 357  
Asp Cys Glu Gly Ser Cys Thr Met Trp  
70 75

ccatctgaca tcaccactct cctcttcaga ggcttcaagg cttttgtttt ctttttgaat 417

aatctttacg agtaaacaaa taagtagact agcgcggtttt tttccctttg agaaatcaat 477

gatggaggta aatagcttcc tattttgtct tattcaataa agaacttatc ataata 533

<210> 25  
<211> 76  
<212> PRT  
<213> Conus textile

<400> 25  
Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser  
1 5 10 15

Thr Gln Ala Leu Val Glu Arg Ala Gly Glu Asn His Ser Lys Glu Asn  
20 25 30

Ile Asn Phe Leu Leu Lys Arg Lys Arg Ala Ala Asp Arg Gly Met Trp  
35 40 45

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Gly Glu Cys Lys Asp Gly Leu Thr Thr Cys Leu Ala Pro Ser Glu Cys  
50 55 60

Cys Ser Glu Asp Cys Glu Gly Ser Cys Thr Met Trp  
65 70 75

<210> 26  
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<212> DNA  
<213> Conus gloriamaris

<220>  
<221> CDS  
<222> (2)..(211)

<400> 26  
g ctg aca atc ctg ctt ctt gtt gct gct gta ctg atg tcg acc cag gcc 49  
Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser Thr Gln Ala  
1 5 10 15

ctg att caa ggt ggt ggt gac aaa cgt caa aag gca aac atc aac ttt 97  
Leu Ile Gln Gly Gly Gly Asp Lys Arg Gln Lys Ala Asn Ile Asn Phe  
20 25 30

ctt tca agg tgg gac cgt gag tgc agg gct tgg tat gcg ccg tgt agc 145  
Leu Ser Arg Trp Asp Arg Glu Cys Arg Ala Trp Tyr Ala Pro Cys Ser  
35 40 45

cct ggc gcg caa tgt tgt agt ttg ctg atg tgt tca aaa gcg acc agc 193  
Pro Gly Ala Gln Cys Cys Ser Leu Leu Met Cys Ser Lys Ala Thr Ser  
50 55 60

cgc tgc ata ttg gcg tta tgaactctga ccacaagcca tccgacatca 241  
Arg Cys Ile Leu Ala Leu  
65 70

ccactctcct cttcagaggc ttcaaggctt tttgtttttc ttttgaagaa tctttacgag 301

tgaacaaata agtagaatag cacgtttttc cccctttgca aaatcaataa tggagggttaa 361

aaaaaaaactt ctgtcttctt caataaagaa gttatcataa taaaaaa 408

<210> 27  
<211> 70  
<212> PRT  
<213> Conus gloriamaris

<400> 27  
Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser Thr Gln Ala  
1 5 10 15

Leu Ile Gln Gly Gly Gly Asp Lys Arg Gln Lys Ala Asn Ile Asn Phe  
20 25 30

Leu Ser Arg Trp Asp Arg Glu Cys Arg Ala Trp Tyr Ala Pro Cys Ser  
35 40 45

Pro Gly Ala Gln Cys Cys Ser Leu Leu Met Cys Ser Lys Ala Thr Ser  
50 55 60

Arg Cys Ile Leu Ala Leu  
65 70

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<210> 28  
 <211> 278  
 <212> DNA  
 <213> Conus marmoreus

<220>  
 <221> CDS  
 <222> (4)..(222)

<400> 28  
 atc atg cag aaa ctg ata atc ctg ctt ctt gtt gct gct gtg ctg ctg 48  
     Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Leu  
       1                  5                  10                  15  
 tcg acc cag gcc cta aat caa gaa aaa cgc cca aag gag atg atc aat 96  
     Ser Thr Gln Ala Leu Asn Gln Glu Lys Arg Pro Lys Glu Met Ile Asn  
                   20                  25                  30  
 ttt tta tca aaa gga aag aca aat gct gag agg cgg aac ggc caa tgc 144  
     Phe Leu Ser Lys Gly Lys Thr Asn Ala Glu Arg Arg Asn Gly Gln Cys  
                   35                  40                  45  
 gag gat gtt tgg atg cct tgt aca tcg aac tgg gaa tgc tgt tct ttg 192  
     Glu Asp Val Trp Met Pro Cys Thr Ser Asn Trp Glu Cys Cys Ser Leu  
           50                  55                  60  
 gat tgt gaa atg tac tgc aca cag ata gga tgaactctga ccacaagcca 242  
     Asp Cys Glu Met Tyr Cys Thr Gln Ile Gly  
       65                  70  
 tccgacatca ccactctcct cttcagagtc ttcaag 278

<210> 29  
 <211> 73  
 <212> PRT  
 <213> Conus marmoreus

<400> 29  
 Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Leu Ser  
     1                  5                  10                  15  
 Thr Gln Ala Leu Asn Gln Glu Lys Arg Pro Lys Glu Met Ile Asn Phe  
           20                  25                  30  
 Leu Ser Lys Gly Lys Thr Asn Ala Glu Arg Arg Asn Gly Gln Cys Glu  
           35                  40                  45  
 Asp Val Trp Met Pro Cys Thr Ser Asn Trp Glu Cys Cys Ser Leu Asp  
       50                  55                  60  
 Cys Glu Met Tyr Cys Thr Gln Ile Gly  
     65                  70

<210> 30  
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 <212> DNA  
 <213> Conus marmoreus

<220>  
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 <222> (4)..(231)

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<400> 30  
 atc atg gag aaa ctg aca atc ctg ctt ctt gtt gct gct gta ctg ata 48  
     Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Ile  
       1                    5                    10                    15

ccg acc cag gcc ctt ttt caa ggt gat gac gga aaa tcc cag aag gcg 96  
 Pro Thr Gln Ala Leu Phe Gln Gly Asp Asp Gly Lys Ser Gln Lys Ala  
                     20                    25                    30

gag atc aag tct ttt gaa aca aga aag tta gcg aga aac aag cag gta 144  
 Glu Ile Lys Ser Phe Glu Thr Arg Lys Leu Ala Arg Asn Lys Gln Val  
                     35                    40                    45

cgc tgc ggt ggt tgg tca acg tat tgt gaa gtt gac gag gaa tgc tgt 192  
 Arg Cys Gly Gly Trp Ser Thr Tyr Cys Glu Val Asp Glu Glu Cys Cys  
                     50                    55                    60

tcg gaa tca tgt gta agg tct tac tgc acg ctg ttt gga tgaactcgga 241  
 Ser Glu Ser Cys Val Arg Ser Tyr Cys Thr Leu Phe Gly  
       65                    70                    75

ccacaagcca tccgatatca ccactctcct gttcagagtc ttcaag 287

<210> 31  
 <211> 76  
 <212> PRT  
 <213> Conus marmoreus

<400> 31  
 Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Ile Pro  
     1                    5                    10                    15

Thr Gln Ala Leu Phe Gln Gly Asp Asp Gly Lys Ser Gln Lys Ala Glu  
                     20                    25                    30

Ile Lys Ser Phe Glu Thr Arg Lys Leu Ala Arg Asn Lys Gln Val Arg  
                     35                    40                    45

Cys Gly Gly Trp Ser Thr Tyr Cys Glu Val Asp Glu Glu Cys Cys Ser  
       50                    55                    60

Glu Ser Cys Val Arg Ser Tyr Cys Thr Leu Phe Gly  
       65                    70                    75

<210> 32  
 <211> 278  
 <212> DNA  
 <213> Conus marmoreus

<220>  
 <221> CDS  
 <222> (4)..(213)

<400> 32  
 atc atg cag aaa ctg ata att ctg ctt ctt gtt gct gct gtg ctg atg 48  
     Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met  
       1                    5                    10                    15

acg acc cag gcc cta tat caa gaa aaa cgc cga aag gag atg atc aat 96  
 Thr Thr Gln Ala Leu Tyr Gln Glu Lys Arg Arg Lys Glu Met Ile Asn  
                     20                    25                    30

0010955125607260



ttt tta tca aaa gga aag ata aat gct gag agg cgg aac ggc gga tgc 144  
Phe Leu Ser Lys Gly Lys Ile Asn Ala Glu Arg Arg Asn Gly Gly Cys  
35 40 45

aaa gct act tgg atg tct tgt tca tgc ggc tgg gaa tgc tgt tct atg 192  
Lys Ala Thr Trp Met Ser Cys Ser Ser Gly Trp Glu Cys Cys Ser Met  
50 55 60

agt tgt gac atg tac tgc gga tagataggat gaactctgac cacaagccat 243  
Ser Cys Asp Met Tyr Cys Gly  
65 70

ccgacatcac cactctcctc ttcagagtct tcaag 278

<210> 33  
<211> 70  
<212> PRT  
<213> Conus marmoreus

<400> 33  
Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met Thr  
1 5 10 15

Thr Gln Ala Leu Tyr Gln Glu Lys Arg Arg Lys Glu Met Ile Asn Phe  
20 25 30

Leu Ser Lys Gly Lys Ile Asn Ala Glu Arg Arg Asn Gly Gly Cys Lys  
35 40 45

Ala Thr Trp Met Ser Cys Ser Ser Gly Trp Glu Cys Cys Ser Met Ser  
50 55 60

Cys Asp Met Tyr Cys Gly  
65 70

<210> 34  
<211> 528  
<212> DNA  
<213> Conus textile

<220>  
<221> CDS  
<222> (98)..(316)

<400> 34  
gcacgtcatc ttctctctca gtctgcctga cagctgcctt cagtcaaccc tgccgtcatc 60

tcacgcgtaga cttggtaaga agtgaaaaac atttatac atg cag aaa ctg ata atc 115  
Met Gln Lys Leu Ile Ile  
1 5

ctg ctt ctt gtt gct gct gtg ctg atg tgc acc cag gcc gtg ctt caa 163  
Leu Leu Leu Val Ala Val Leu Met Ser Thr Gln Ala Val Leu Gln  
10 15 20

gaa aaa cgc cca aag gag aag atc aag ctt tta tca aag aga aag aca 211  
Glu Lys Arg Pro Lys Glu Lys Ile Lys Leu Leu Ser Lys Arg Lys Thr  
25 30 35

gat gct gag aag cag cag-aag cgc ctt tgc ccg gat tac-acg gag-cct- 259  
Asp Ala Glu Lys Gln Gln Lys Arg Leu Cys Pro Asp Tyr Thr Glu Pro  
40 45 50

0910951-121598

tgt tca cat gcc cat gaa tgc tgt tca tgg aat tgt tat aat ggg cac 307  
Cys Ser His Ala His Glu Cys Cys Ser Trp Asn Cys Tyr Asn Gly His  
55 60 65 70

tgt acg gga tgaactcgga ccacaagcca tccgacatca ccactctcct 356  
Cys Thr Gly

cttcagaggc ttcaagactt ttgttctgat tttggacaat ctttacgagt aaacaaataa 416

ttagactagc acttttttttc ccctttgcaa aatcaatgat ggaggtaaaa agcctcccat 476

tttgtcttca tcaataaaga acttatcatc aaaaaaaaaa aaaaaaaaaa aa 528

<210> 35  
<211> 73  
<212> PRT  
<213> Conus textile

<400> 35  
Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser  
1 5 10 15

Thr Gln Ala Val Leu Gln Glu Lys Arg Pro Lys Glu Lys Ile Lys Leu  
20 25 30

Leu Ser Lys Arg Lys Thr Asp Ala Glu Lys Gln Gln Lys Arg Leu Cys  
35 40 45

Pro Asp Tyr Thr Glu Pro Cys Ser His Ala His Glu Cys Cys Ser Trp  
50 55 60

Asn Cys Tyr Asn Gly His Cys Thr Gly  
65 70

<210> 36  
<211> 26  
<212> PRT  
<213> Conus textile

<220>  
<221> PEPTIDE  
<222> (1)..(26)  
<223> Xaa at residue 18 is Trp or 6-bromo-Trp; Xaa at  
residues 7 and 14 are Glu or  
gamma-carboxyglutamate; Xaa at residues 3 and 8  
are Pro or hydroxy-Pro.

<400> 36  
Leu Cys Xaa Asp Tyr Thr Xaa Xaa Cys Ser His Ala His Xaa Cys Cys  
1 5 10 15

Ser Xaa Asn Cys Tyr Asn Gly His Cys Thr  
20 25

<210> 37  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:consensus

0961095-14598

gamma-conopeptide sequence for probe

<220>  
<221> PEPTIDE  
<222> (1)  
<223> Xaa is Glu or Gln.

<400> 37  
Xaa Cys Cys Ser  
1

<210> 38  
<211> 12  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:degenerate  
probe for consensus gamma-conopeptide sequence.

<400> 38  
sartgytggya gy

12

<210> 39  
<211> 12  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:degenerate  
probe for consensus gamma-conopeptide sequence.

<400> 39  
sartgytgyt cn

12

<210> 40  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:consensus  
pro-gamma-conopeptide sequence for probe.

<400> 40  
Ile Leu Leu Val Ala Ala Val Leu  
1 5

<210> 41  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:degenerate  
probe for consensus pro-gamma-conopeptide  
sequence.

<400> 41  
athytnytng tngcngcngt nytn

24

09210952.121593

<210> 42  
 <211> 31  
 <212> PRT  
 <213> Conus pennaceus

<220>  
 <221> PEPTIDE  
 <222> (1)..(31)  
 <223> Xaa at residues 14 and 26 are  
 gamma-carboxyglutamate; Xaa at residue 31 is  
 hdroxy-Pro.

<400> 42  
 Asp Cys Thr Ser Trp Phe Gly Arg Cys Thr Val Asn Ser Xaa Cys Cys  
           1                          5                          10                          15  
 Ser Asn Ser Cys Asp Gln Thr Tyr Cys Xaa Leu Tyr Ala Phe Xaa Ser  
                           20                          25                          30

<210> 43  
 <211> 27  
 <212> PRT  
 <213> Conus textile

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residues 9 and 13 are  
 gamma-carboxyglutamate.

<400> 43  
 Cys Gly Gly Tyr Ser Thr Tyr Cys Xaa Val Asp Ser Xaa Cys Cys Ser  
           1                          5                          10                          15  
 Asp Asn Cys Val Arg Ser Tyr Cys Thr Leu Phe  
                           20                          25

<210> 44  
 <211> 8  
 <212> PRT  
 <213> Conus pennaceus

<220>  
 <221> MOD\_RES  
 <222> (2)  
 <223> Xaa at residue 2 is carboxymethylCys

<400> 44  
 Asp Xaa Thr Ser Trp Phe Gly Arg  
           1                          5

<210> 45  
 <211> 24  
 <212> PRT  
 <213> Conus pennaceus

<220>  
 <221> PEPTIDE  
 <222> (1)..(24)  
 <223> Xaa at residues 6 and 18 are

0021095.121598

gamma-carboxyglutamate; Xaa at residue 23 is hydroxy-Pro.

<400> 45  
Xaa Thr Val Asn Ser Xaa Xaa Xaa Ser Asn Ser Xaa Asp Gln Thr Tyr  
1 5 10 15

Xaa Xaa Leu Tyr Ala Phe Xaa Ser  
20

<210> 46  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer for M13  
universal priming site.

<400> 46  
tttcccagtc acgacgtt 18

<210> 47  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer for M13  
reverse priming site.

<400> 47  
cacacaggaa acagctatg 19

09210952-12198